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RAW SEQUENCE LISTING

DATE: 07/30/2004

PATENT APPLICATION: US/10/502,279

TIME: 09:32:53

Input Set : A:\Q82704 Sequence Listing.txt

Output Set: N:\CRF4\07302004\J502279.raw

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3 <110> APPLICANT: Yamanouchi Pharmaceutical Co., Ltd.
4     Hideki ENDOH
5     Ryosuke NAKANO
6     Eiji KUROSAKI
7     Miyuki KATO
8     Hiroyuki YOKOTA
9     Kazunori INABE
11 <120> TITLE OF INVENTION: METHOD FOR SCREENING A DRUG AMELIORATING INSULIN RESISTANCE
13 <130> FILE REFERENCE: Q82704
C--> 15 <140> CURRENT APPLICATION NUMBER: US/10/502,279
C--> 15 <141> CURRENT FILING DATE: 2004-07-23
15 <150> PRIOR APPLICATION NUMBER: JP 2002-013721
16 <151> PRIOR FILING DATE: 2002-01-23
18 <150> PRIOR APPLICATION NUMBER: JP 2002-257703
19 <151> PRIOR FILING DATE: 2002-09-03
21 <160> NUMBER OF SEQ ID NOS: 28
23 <170> SOFTWARE: PatentIn version 3.1
25 <210> SEQ ID NO: 1
26 <211> LENGTH: 1518
27 <212> TYPE: DNA
28 <213> ORGANISM: Homo sapiens
30 <220> FEATURE:
31 <221> NAME/KEY: CDS
32 <222> LOCATION: (1)..(1518)
33 <223> OTHER INFORMATION:
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38 Met Gly Glu Thr Leu Gly Asp Ser Pro Ile Asp Pro Glu Ser Asp Ser
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41 ttc act gat aca ctg tct gca aac ata tca caa gaa atg acc atg gtt      96
42 Phe Thr Asp Thr Leu Ser Ala Asn Ile Ser Gln Glu Met Thr Met Val
43           20           25           30
45 gac aca gag atg cca ttc tgg ccc acc aac ttt ggg atc agc tcc gtg      144
46 Asp Thr Glu Met Pro Phe Trp Pro Thr Asn Phe Gly Ile Ser Ser Val
47           35           40           45
49 gat ctc tcc gta atg gaa gac cac tcc cac tcc ttt gat atc aag ccc      192
50 Asp Leu Ser Val Met Glu Asp His Ser His Ser Phe Asp Ile Lys Pro
51           50           55           60
53 ttc act act gtt gac ttc tcc agc att tct act cca cat tac gaa gac      240
54 Phe Thr Thr Val Asp Phe Ser Ser Ile Ser Thr Pro His Tyr Glu Asp
55 65           70           75           80
57 att cca ttc aca aga aca gat cca gtg gtt gca gat tac aag tat gac      288
58 Ile Pro Phe Thr Arg Thr Asp Pro Val Val Ala Asp Tyr Lys Tyr Asp

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59	85	90	95	
61	ctg aaa ctt caa gag tac caa agt gca atc aaa gtg gag cct gca tct	336		
62	Leu Lys Leu Gln Glu Tyr Gln Ser Ala Ile Lys Val Glu Pro Ala Ser			
63	100 105 110			
65	cca cct tat tat tct gag aag act cag ctc tac aat aag cct cat gaa	384		
66	Pro Pro Tyr Tyr Ser Glu Lys Thr Gln Leu Tyr Asn Lys Pro His Glu			
67	115 120 125			
69	gag cct tcc aac tcc ctc atg gca att gaa tgt cgt gtc tgt gga gat	432		
70	Glu Pro Ser Asn Ser Leu Met Ala Ile Glu Cys Arg Val Cys Gly Asp			
71	130 135 140			
73	aaa gct tct gga ttt cac tat gga gtt cat gct tgt gaa gga tgc aag	480		
74	Lys Ala Ser Gly Phe His Tyr Gly Val His Ala Cys Glu Gly Cys Lys			
75	145 150 155 160			
77	ggt ttc ttc cgg aga aca atc aga ttg aag ctt atc tat gac aga tgt	528		
78	Gly Phe Phe Arg Arg Thr Ile Arg Leu Lys Leu Ile Tyr Asp Arg Cys			
79	165 170 175			
81	gat ctt aac tgt cgg atc cac aaa aaa agt aga aat aaa tgt cag tac	576		
82	Asp Leu Asn Cys Arg Ile His Lys Lys Ser Arg Asn Lys Cys Gln Tyr			
83	180 185 190			
85	tgt cgg ttt cag aaa tgc ctt gca gtg ggg atg tct cat aat gcc atc	624		
86	Cys Arg Phe Gln Lys Cys Leu Ala Val Gly Met Ser His Asn Ala Ile			
87	195 200 205			
89	agg ttt ggg cgg atg cca cag gcc gag aag gag aag ctg ttg gcg gag	672		
90	Arg Phe Gly Arg Met Pro Gln Ala Glu Lys Glu Lys Leu Leu Ala Glu			
91	210 215 220			
93	atc tcc agt gat atc gac cag ctg aat cca gag tcc gct gac ctc cgg	720		
94	Ile Ser Ser Asp Ile Asp Gln Leu Asn Pro Glu Ser Ala Asp Leu Arg			
95	225 230 235 240			
97	gcc ctg gca aaa cat ttg tat gac tca tac ata aag tcc ttc ccg ctg	768		
98	Ala Leu Ala Lys His Leu Tyr Asp Ser Tyr Ile Lys Ser Phe Pro Leu			
99	245 250 255			
101	acc aaa gca aag gcg agg gcg atc ttg aca gga aag aca aca gac aaa	816		
102	Thr Lys Ala Lys Ala Arg Ala Ile Leu Thr Gly Lys Thr Thr Asp Lys			
103	260 265 270			
105	tca cca ttc gtt atc tat gac atg aat tcc tta atg atg gga gaa gat	864		
106	Ser Pro Phe Val Ile Tyr Asp Met Asn Ser Leu Met Met Gly Glu Asp			
107	275 280 285			
109	aaa atc aag ttc aaa cac atc acc ccc ctg cag gag cag agc aaa gag	912		
110	Lys Ile Lys Phe Lys His Ile Thr Pro Leu Gln Glu Gln Ser Lys Glu			
111	290 295 300			
113	gtg gcc atc cgc atc ttt cag ggc tgc cag ttt cgc tcc gtg gag gct	960		
114	Val Ala Ile Arg Ile Phe Gln Gly Cys Gln Phe Arg Ser Val Glu Ala			
115	305 310 315 320			
117	gtg cag gag atc aca gag tat gcc aaa agc att cct ggt ttt gta aat	1008		
118	Val Gln Glu Ile Thr Glu Tyr Ala Lys Ser Ile Pro Gly Phe Val Asn			
119	325 330 335			
121	ctt gac ttg aac gac caa gta act ctc ctc aaa tat gga gtc cac gag	1056		
122	Leu Asp Leu Asn Asp Gln Val Thr Leu Leu Lys Tyr Gly Val His Glu			
123	340 345 350			

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125 atc att tac aca atg ctg gcc tcc ttg atg aat aaa gat ggg gtt ctc      1104
126 ile ile tyr thr met leu ala ser leu met asn lys asp gly val leu
127          355                      360                      365
129 ata tcc gag ggc caa ggc ttc atg aca agg gag ttt cta aag agc ctg      1152
130 ile ser glu gly gln gly phe met thr arg glu phe leu lys ser leu
131          370                      375                      380
133 cga aag cct ttt ggt gac ttt atg gag ccc aag ttt gag ttt gct gtg      1200
134 arg lys pro phe gly asp phe met glu pro lys phe glu phe ala val
135 385          390                      395                      400
137 aag ttc aat gca ctg gaa tta gat gac agc gac ttg gca ata ttt att      1248
138 lys phe asn ala leu glu leu asp asp ser asp leu ala ile phe ile
139          405                      410                      415
141 gct gtc att att ctc agt gga gac cgc cca ggt ttg ctg aat gtg aag      1296
142 ala val ile ile leu ser gly asp arg pro gly leu leu asn val lys
143          420                      425                      430
145 ccc att gaa gac att caa gac aac ctg cta caa gcc ctg gag ctc cag      1344
146 pro ile glu asp ile gln asp asn leu leu gln ala leu glu leu gln
147          435                      440                      445
149 ctg aag ctg aac cac cct gag tcc tca cag ctg ttt gcc aag ctg ctc      1392
150 leu lys leu asn his pro glu ser ser gln leu phe ala lys leu leu
151          450                      455                      460
153 cag aaa atg aca gac ctc aga cag att gtc acg gaa cac gtg cag cta      1440
154 gln lys met thr asp leu arg gln ile val thr glu his val gln leu
155 465          470                      475                      480
157 ctg cag gtg atc aag aag acg gag aca gac atg agt ctt cac ccg ctc      1488
158 leu gln val ile lys lys thr glu thr asp met ser leu his pro leu
159          485                      490                      495
161 ctg cag gag atc tac aag gac ttg tac tag      1518
162 leu gln glu ile tyr lys asp leu tyr
163          500                      505
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167 <211> LENGTH: 505
168 <212> TYPE: PRT
169 <213> ORGANISM: Homo sapiens
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174 1          5          10          15
177 Phe Thr Asp Thr Leu Ser Ala Asn Ile Ser Gln Glu Met Thr Met Val
178          20          25          30
181 Asp Thr Glu Met Pro Phe Trp Pro Thr Asn Phe Gly Ile Ser Ser Val
182          35          40          45
185 Asp Leu Ser Val Met Glu Asp His Ser His Ser Phe Asp Ile Lys Pro
186          50          55          60
189 Phe Thr Thr Val Asp Phe Ser Ser Ile Ser Thr Pro His Tyr Glu Asp
190 65          70          75          80
193 Ile Pro Phe Thr Arg Thr Asp Pro Val Val Ala Asp Tyr Lys Tyr Asp
194          85          90          95
197 Leu Lys Leu Gln Glu Tyr Gln Ser Ala Ile Lys Val Glu Pro Ala Ser
198          100          105          110

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201 Pro Pro Tyr Tyr Ser Glu Lys Thr Gln Leu Tyr Asn Lys Pro His Glu
202      115      120      125
205 Glu Pro Ser Asn Ser Leu Met Ala Ile Glu Cys Arg Val Cys Gly Asp
206      130      135      140
209 Lys Ala Ser Gly Phe His Tyr Gly Val His Ala Cys Glu Gly Cys Lys
210 145      150      155      160
213 Gly Phe Phe Arg Arg Thr Ile Arg Leu Lys Leu Ile Tyr Asp Arg Cys
214      165      170      175
217 Asp Leu Asn Cys Arg Ile His Lys Lys Ser Arg Asn Lys Cys Gln Tyr
218      180      185      190
221 Cys Arg Phe Gln Lys Cys Leu Ala Val Gly Met Ser His Asn Ala Ile
222      195      200      205
225 Arg Phe Gly Arg Met Pro Gln Ala Glu Lys Glu Lys Leu Leu Ala Glu
226      210      215      220
229 Ile Ser Ser Asp Ile Asp Gln Leu Asn Pro Glu Ser Ala Asp Leu Arg
230 225      230      235      240
233 Ala Leu Ala Lys His Leu Tyr Asp Ser Tyr Ile Lys Ser Phe Pro Leu
234      245      250      255
237 Thr Lys Ala Lys Ala Arg Ala Ile Leu Thr Gly Lys Thr Thr Asp Lys
238      260      265      270
241 Ser Pro Phe Val Ile Tyr Asp Met Asn Ser Leu Met Met Gly Glu Asp
242      275      280      285
245 Lys Ile Lys Phe Lys His Ile Thr Pro Leu Gln Glu Gln Ser Lys Glu
246      290      295      300
249 Val Ala Ile Arg Ile Phe Gln Gly Cys Gln Phe Arg Ser Val Glu Ala
250 305      310      315      320
253 Val Gln Glu Ile Thr Glu Tyr Ala Lys Ser Ile Pro Gly Phe Val Asn
254      325      330      335
257 Leu Asp Leu Asn Asp Gln Val Thr Leu Leu Lys Tyr Gly Val His Glu
258      340      345      350
261 Ile Ile Tyr Thr Met Leu Ala Ser Leu Met Asn Lys Asp Gly Val Leu
262      355      360      365
265 Ile Ser Glu Gly Gln Gly Phe Met Thr Arg Glu Phe Leu Lys Ser Leu
266      370      375      380
269 Arg Lys Pro Phe Gly Asp Phe Met Glu Pro Lys Phe Glu Phe Ala Val
270 385      390      395      400
273 Lys Phe Asn Ala Leu Glu Leu Asp Asp Ser Asp Leu Ala Ile Phe Ile
274      405      410      415
277 Ala Val Ile Ile Leu Ser Gly Asp Arg Pro Gly Leu Leu Asn Val Lys
278      420      425      430
281 Pro Ile Glu Asp Ile Gln Asp Asn Leu Leu Gln Ala Leu Glu Leu Gln
282      435      440      445
285 Leu Lys Leu Asn His Pro Glu Ser Ser Gln Leu Phe Ala Lys Leu Leu
286      450      455      460
289 Gln Lys Met Thr Asp Leu Arg Gln Ile Val Thr Glu His Val Gln Leu
290 465      470      475      480
293 Leu Gln Val Ile Lys Lys Thr Glu Thr Asp Met Ser Leu His Pro Leu
294      485      490      495
297 Leu Gln Glu Ile Tyr Lys Asp Leu Tyr

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298          500          505
301 <210> SEQ ID NO: 3
302 <211> LENGTH: 987
303 <212> TYPE: DNA
304 <213> ORGANISM: Homo sapiens
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307 <221> NAME/KEY: CDS
308 <222> LOCATION: (1)..(987)
309 <223> OTHER INFORMATION:
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313 Met Ala Ala Gly Ile Val Ala Ser Arg Arg Leu Arg Asp Leu Leu Thr
314 1          5          10          15
316 cgg cga ctg aca ggc tcc aac tac ccg gga ctc agt att agc ctt cgc      96
317 Arg Arg Leu Thr Gly Ser Asn Tyr Pro Gly Leu Ser Ile Ser Leu Arg
318          20          25          30
320 ctc act ggc tcc tct gca caa gag gcg gct tcc gga gta gcc ctc ggt      144
321 Leu Thr Gly Ser Ser Ala Gln Glu Ala Ala Ser Gly Val Ala Leu Gly
322          35          40          45
324 gaa gcc cca gac cac agc tat gag tcc ctt cgt gtg acg tct gcg cag      192
325 Glu Ala Pro Asp His Ser Tyr Glu Ser Leu Arg Val Thr Ser Ala Gln
326          50          55          60
328 aaa cat gtt ctg cat gtc cag ctc aac cgg ccc aac aag agg aat gcc      240
329 Lys His Val Leu His Val Gln Leu Asn Arg Pro Asn Lys Arg Asn Ala
330 65          70          75          80
332 atg aac aag gtc ttc tgg aga gag atg gta gag tgc ttc aac aag att      288
333 Met Asn Lys Val Phe Trp Arg Glu Met Val Glu Cys Phe Asn Lys Ile
334          85          90          95
336 tcg aga gac gct gac tgt cgg gcg gtg gtg atc tct ggt gca gga aaa      336
337 Ser Arg Asp Ala Asp Cys Arg Ala Val Val Ile Ser Gly Ala Gly Lys
338          100          105          110
340 atg ttc act gca ggt att gac ctg atg gac atg gct tcg gac atc ctg      384
341 Met Phe Thr Ala Gly Ile Asp Leu Met Asp Met Ala Ser Asp Ile Leu
342          115          120          125
344 cag ccc aaa gga gat gat gtg gcc cgg atc agc tgg tac ctc cgt gac      432
345 Gln Pro Lys Gly Asp Asp Val Ala Arg Ile Ser Trp Tyr Leu Arg Asp
346          130          135          140
348 atc atc act cga tac cag gag acc ttc aac gtc atc gag agg tgc ccc      480
349 Ile Ile Thr Arg Tyr Gln Glu Thr Phe Asn Val Ile Glu Arg Cys Pro
350 145          150          155          160
352 aag ccc gtg att gct gcc gtc cat ggg ggc tgc att ggc gga ggt gtg      528
353 Lys Pro Val Ile Ala Ala Val His Gly Gly Cys Ile Gly Gly Gly Val
354          165          170          175
356 gac ctt gtc acc gcc tgt gac atc cgg tac tgt gcc cag gat gct ttc      576
357 Asp Leu Val Thr Ala Cys Asp Ile Arg Tyr Cys Ala Gln Asp Ala Phe
358          180          185          190
360 ttc cag gtg aag gag gtg gac gtg ggt ttg gct gcc gat gta gga aca      624
361 Phe Gln Val Lys Glu Val Asp Val Gly Leu Ala Ala Asp Val Gly Thr
362          195          200          205

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VERIFICATION SUMMARY

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Input Set : A:\Q82704 Sequence Listing.txt

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L:15 M:270 C: Current Application Number differs, Replaced Current Application No
L:15 M:271 C: Current Filing Date differs, Replaced Current Filing Date
L:36 M:258 W: Mandatory Feature missing, <223> Blank for SEQ#:1,Line#:33
L:311 M:258 W: Mandatory Feature missing, <223> Blank for SEQ#:3,Line#:309
L:498 M:258 W: Mandatory Feature missing, <223> Blank for SEQ#:5,Line#:496
L:757 M:258 W: Mandatory Feature missing, <223> Blank for SEQ#:7,Line#:755
L:970 M:258 W: Mandatory Feature missing, <223> Blank for SEQ#:16,Line#:968
L:1219 M:258 W: Mandatory Feature missing, <223> Blank for SEQ#:26,Line#:1217